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Dear Aaron,

You ask in your letter of October 21st how I arrived at my interpretation of your suggestion for the packing of the crystals. The argument went as follows.

I assumed that there had to be one dyad axis. For simplicity I chose this to be the shorter; that is, along a . Thus one nucleosome had its dyad exactly parallel to a . To bring the DNA helices of the other two into phase with the first one and to give an arrangement which looks roughly like 6 turns in the 340 Å repeat one needs to put their dyads roughly parallel to the first one. (Naturally if they are exactly parallel one gets a shorter repeat.) I then assumed that the relationship of these two dyads to each other might be the same as the relationship in a solenoid with about 6 nucleosomes per turn. This implies that the dyads would have an angle of about 60° between them. One can get this by tipping one up 30° and the other down 30° .

I don't accept your screwing-down argument because I can see no strong reason why the nucleosomes should be screwed down in the crystal packing. What is necessary to give the sort of pattern you have is that the DNA in the nucleosomes should everywhere be not far from a regular helix with about 6 turns - or so I surmise if I have remembered the diffraction pattern more or less correctly. However, there is no reason to suppose that even the DNA in one nucleosome accurately follows a helix. I could have the ends splayed up or splayed down, as explained in my earlier note. Clearly the DNA "helix" in the crystal is unlikely to be completely regular or you would have no spots on the axis.

My feeling is that there are so many degrees of freedom that however good a guess you make only an isomorphous replacement can decide the issue.

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About the density. Lubert Stryer, who is now Professor of Anatomy at the Medical School at Stanford, says he can measure the density of small crystals. Basically, you pop them in a density gradient and try to catch a view of them immediately using a microscope, before they have had time to alter. Why not write to him for details. I think it most rash to try to solve the ~~structures~~ without the density. He says, incidentally, he can measure to 1 or 2% which is more than adequate.

A short memorandum on the final fold ~~as~~ enclosed. I am also sending a copy to Bak. I have a picture from Bak of a cross-section (copy enclosed). It indeed is hollow. It shows a 300 Å fibre but very irregular and kinky. Of course this may be an artifact. We shall have to wait and see what further pictures look like.

It occurs to me that you and Bak should really meet for a proper discussion. Either you should invite him to Cambridge - perhaps EMBO would provide the money. Why shouldn't he come to exchange techniques, for example? Or you should make, in the near future, one of your trips to Aarhus. I feel this tri-party correspondence is becoming absurd!